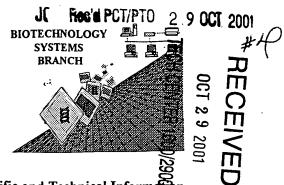Barbara
Campbell

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/889,182_

Source: _1600 RUSH_

Date Processed by STIC: _10/22/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE**
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1600

RAW SEQUENCE LISTING   DATE: 10/22/2001
PATENT APPLICATION: US/09/889,182   TIME: 12:13:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\10222001\I889182.raw

all U.S.
application
must be in
English

Does Not Comply
Corrected Diskette Needed

pp 1,4

```
W-->  1 (SEQUENZPROTOKOLL) delete
    , 4 <110> APPLICANT: Deutsches Krebsforschungszentrum
      6 <120> TITLE OF INVENTION: (Selektion von monoklonalen Antikrpern)
      8 <130> FILE REFERENCE: K 2779
OK-> 10 <140> CURRENT APPLICATION NUMBER: US/09/889,182
     11 <141> CURRENT FILING DATE: 2000-01-11
     13 <150> PRIOR APPLICATION NUMBER: DE 199 00 635.0-41
     14 <151> PRIOR FILING DATE: 1999-01-11
     16 <160> NUMBER OF SEQ ID NOS: 6
     18 <170> SOFTWARE: PatentIn Ver. 2.1.
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 5732
     23 <212> TYPE: DNA
     24 <213> ORGANISM: (knstliche Sequenz)
     26 <220> FEATURE:
     27 <221> NAME/KEY: CDS
     28 <222> LOCATION: (737) ... (1420)
     29 <223> OTHER INFORMATION: (Beschreibung der knstlichen Sequenz: Antikrper-Bindeprotein
     32 <400> SEQUENCE: 1
     35 gcgcgcgttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag     60
     37 ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct    120
     39 gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc    180
     41 caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg    240
     43 cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat    300
     45 ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca    360
     47 tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc    420
     49 gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga    480
     51 gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat    540
     53 tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctctctggc    600
     55 taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga    660
     57 cccaagcttg gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg    720
     59 cttggggata tccacc atg gag aca gac aca ctc ctg cta tgg gta ctg         769
     60                    Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu
     61                     1               5                   10
     63 ctg ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca      817
     64 Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro
     65            15                   20                  25
     67 gat tat gct ggg gcc caa aag ccc gag gtg atc gat gcc agc gag ctg      865
     68 Asp Tyr Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu
     69            30                   35                  40
     71 acc ccc gcc gtg acc acc tac aag cta gtg atc aac ggc aag acc ctg      913
     72 Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu
     73        45                   50                  55
     75 aag ggc gag acc acc acc gag gcc gtg gac gcc gcc acc gcg gag aag      961
     76 Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys
     77     60                   65                  70                  75
     79 gtg ttc aaa caa tac gct aat gac aac ggg gtc gac ggc gag tgg act     1009
```

```
80  Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr
81                  80                  85                  90
83  tac gac gac gcc acc aag acc ttc acc gtg acc gag aag ccc gag gtg      1057
84  Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val
85                  95                 100                 105
87  atc gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag cta gtg      1105
88  Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val
89          110                 115                 120
91  atc aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc gtg gac      1153
92  Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp
93      125                 130                 135
95  gcc gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac aac ggg      1201
96  Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly
97  140                 145                 150                 155
99  gtc gac ggc gag tgg act tac gac gac gcc acc aag acc ttc acc gtg      1249
100 Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val
101                 160                 165                 170
103 acc gag gcg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat      1297
104 Thr Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
105             175                 180                 185
107 ggg gcc gtc gac gga caa aac gac acc agc caa acc agc agc ccc tca      1345
108 Gly Ala Val Asp Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
109         190                 195                 200
111 gca tcc agc aac ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat      1393
112 Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn
113         205                 210                 215
115 gcc ata atc cac ctc ttc tgc ttc agt tgaggtgaca cgtctagagc           1440
116 Ala Ile Ile His Leu Phe Cys Phe Ser
117 220                 225
119 tattctatag tgtcacctaa atgctagagc tcgctgatca gcctcgactg tgccttctag   1500
121 ttgccagcca tctgttgttt gcccctcccc cgtgccttcc ttgaccctgg aaggtgccac   1560
123 tcccactgtc ctttcctaat aaaatgagga aattgcatcg cattgtctga gtaggtgtca   1620
125 ttctattctg gggggtgggg tggggcagga cagcaagggg gaggattggg aagacaatag   1680
127 caggcatgct ggggatgcgg tgggctctat ggcttctgag gcggaaagaa ccagtggcgg   1740
129 taatacggtt atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc   1800
131 agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc gttttttcat aggctccgcc   1860
133 cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac   1920
136 tataaagata ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc   1980
138 tgccgcttac cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata   2040
140 gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc   2100
142 acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca   2160
144 acccggtaag acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag   2220
146 cgaggtatgt aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta   2280
148 gaaggacagt atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg   2340
150 gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc   2400
152 agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt   2460
154 ctgacgctca gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcaaaaa   2520
156 ggatcttcac ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat   2580
158 atgagtaacc tgaggctatg gcagggcctg ccgccccgac gttggctgcg agccctgggc   2640
```

RAW SEQUENCE LISTING   DATE: 10/22/2001
PATENT APPLICATION: US/09/889,182   TIME: 12:13:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\10222001\I889182.raw

```
160 cttcacccga acttgggggg tggggtgggg aaaaggaaga aacgcgggcg tattggcccc 2700
162 aatgggtct cggtggggta tcgacagagt gccagccctg ggaccgaacc ccgcgtttat 2760
164 gaacaaacga cccaacaccg tgcgttttat tctgtctttt tattgccgtc atagcgcggg 2820
166 ttccttccgg tattgtctcc ttccgtgttt cagttagcct cccctaggg tgggcgaaga 2880
168 actccagcat gagatccccg cgctggagga tcatccagcc ggcgtcccgg aaaacgattc 2940
170 cgaagcccaa cctttcatag aaggcggcgg tggaatcgaa atctcgtgat ggcaggttgg 3000
172 gcgtcgcttg gtcggtcatt tcgaacccca gagtcccgct cagaagaact cgtcaagaag 3060
174 gcgatagaag gcgatgcgct gcgaatcggg agcggcgata ccgtaaagca cgaggaagcg 3120
176 gtcagcccat tcgccgccaa gctcttcagc aatatcacgg gtagccaacg ctatgtcctg 3180
178 atagcggtcc gccacaccca gccggccaca gtcgatgaat ccagaaaagc ggccattttc 3240
180 caccatgata ttcggcaagc aggcatcgcc atgggtcacg acgagatcct cgccgtcggg 3300
182 catgctcgcc ttgagcctgg cgaacagttc ggctggcgcg agccctgat gctcttgatc 3360
184 atcctgatcg acaagaccgg cttccatccg agtacgtgct cgctcgatgc gatgtttcgc 3420
186 ttggtggtcg aatgggcagg tagccggatc aagcgtatgc agccgccgca ttgcatcagc 3480
188 catgatggat actttctcgg caggagcaag gtgagatgac aggagatcct gccccggcac 3540
190 ttcgcccaat agcagccagt cccttcccgc ttcagtgaca acgtcgagca cagctgcgca 3600
192 aggaacgccc gtcgtggcca gccacgatag ccgcgctgcc tcgtcttgca gttcattcag 3660
194 ggcaccggac aggtcggtct tgacaaaaag aaccgggcgc ccctgcgctg acagccggaa 3720
196 cacggcggca tcagagcagc cgattgtctg ttgtgcccag tcatagccga atagcctctc 3780
198 cacccaagcg gccggagaac ctgcgtgcaa tccatcttgt tcaatcatgc gaaacgatcc 3840
200 tcatcctgtc tcttgatcga tctttgcaaa agcctaggcc tccaaaaaag cctcctcact 3900
202 acttctggaa tagctcagag gccgaggagg cggcctcggc ctctgcataa ataaaaaaaa 3960
205 ttagtcagcc atggggcgga gaatgggcgg aactgggcgg agttaggggc gggatgggcg 4020
207 gagttagggg cgggactatg gttgctgact aattgagatg catgctttgc atacttctgc 4080
209 ctgctgggga gcctggggac tttccacacc tggttgctga ctaattgaga tgcatgcttt 4140
211 gcatacttct gcctgctggg gagcctgggg actttccaca ccctaactga cacacattcc 4200
213 acagctggtt ctttccgcct caggactctt ccttttcaa taaatcaatc taaagtatat 4260
215 atgagtaaac ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga 4320
217 tctgtctatt tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac 4380
219 gggagggctt accatctggc cccagtgctg caatgatacc gcgagaccca cgctcaccgg 4440
221 ctccagattt atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg 4500
223 caactttatc cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt 4560
225 cgccagttaa tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct 4620
227 cgtcgtttgg tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat 4680
229 cccccatgtt gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta 4740
231 agttggccgc agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca 4800
233 tgccatccgt aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat 4860
235 agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac 4920
237 atagcagaac tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa 4980
239 ggatcttacc gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt 5040
241 cagcatcttt tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg 5100
243 caaaaaaggg aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat 5160
245 attattgaag catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt 5220
247 agaaaaataa acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgcgc 5280
249 cctgtagcgg cgcattaagc gcggcgggtg tggtggttac gcgcagcgtg accgctacac 5340
251 ttgccagcgc cctagcgccc gctcctttcg ctttcttccc ttcctttctc gccacgttcg 5400
253 ccggctttcc ccgtcaagct ctaaatcggg ggctcccttt agggttccga tttagtgctt 5460
255 tacggcacct cgaccccaaa aaacttgatt agggtgatgg ttcacgtagt gggccatcgc 5520
257 cctgatagac ggtttttcgc cctttgacgt tggagtccac gttctttaat agtggactct 5580
```

```
RAW SEQUENCE LISTING                    DATE: 10/22/2001
PATENT APPLICATION:  US/09/889,182      TIME: 12:13:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\10222001\I889182.raw
```

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259 tgttccaaac tggaacaaca ctcaacccta tctcggtcta ttcttttgat ttataaggga   5640
261 ttttgccgat ttcggcctat tggttaaaaa atgagctgat ttaacaaaaa tttaacgcga   5700
263 attttaacaa aatattaacg cttacaattt ac                                  5732
267 <210> SEQ ID NO: 2
268 <211> LENGTH: 228
269 <212> TYPE: PRT
270 <213> ORGANISM: knstliche Sequenz                    <220>
272 <223> OTHER INFORMATION: Beschreibung der knstlichen Sequenz: Antikrper-Bindeprotein
274 <400> SEQUENCE: 2
277 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
278   1               5                  10                  15
280 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
281              20                  25                  30
283 Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr
284          35                  40                  45
286 Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr
287     50                  55                  60
289 Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr
290  65                  70                  75                  80
292 Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr
293              85                  90                  95
295 Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu
296          100                 105                 110
298 Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr
299          115                 120                 125
301 Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu
302     130                 135                 140
304 Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp
305 145                 150                 155                 160
307 Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala
308              165                 170                 175
310 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly
311          180                 185                 190
313 Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile
314          195                 200                 205
316 Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu
317     210                 215                 220
319 Phe Cys Phe Ser
320 225
324 <210> SEQ ID NO: 3
325 <211> LENGTH: 6094
326 <212> TYPE: DNA
327 <213> ORGANISM: knstliche Sequenz
329 <220> FEATURE:
330 <221> NAME/KEY: CDS
331 <222> LOCATION: (682) ... (1782)
332 <223> OTHER INFORMATION: Beschreibung der knstlichen Sequenz: Antikrper-Bindeprotein
334 <400> SEQUENCE: 3
337 gcgcgcgttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag   60
```

Handwritten annotations: insert this mandatory numeric identifier wherever <221>, <222>, or <223> is shown. ">< 2207" Please correct any subsequent sequences showing this error.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,182

DATE: 10/22/2001
TIME: 12:13:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\10222001\I889182.raw

```
339 ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct    120
341 gaccgcccaa cgaccccgc  ccattgacgt caataatgac gtatgttccc atagtaacgc    180
343 caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg    240
345 cagtacatca agtgtatcat atgccaagta cgcccccctat tgacgtcaat gacggtaaat    300
347 ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca    360
349 tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc    420
351 gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga    480
353 gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat    540
355 tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctctctggc    600
357 taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga    660
359 cccaagcttg gtaccggtgc g atg gca ccc tgc atg ctg ctc ctg ctg ttg     711
360                         · · Met Ala Pro Cys Met Leu Leu Leu Leu Leu
361                            1            5                      10
364 gcg gcc gcc ctg gcc ccg act cag acc cgc gcg ggg gcc caa aag gag     759
365 Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu
366               15                20                25
368 aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg     807
369 Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
370               30                35                40
372 atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc     855
373 Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
374               45                50                55
376 gag gag gcc acc gcg gag gcc tac cgc tac gcc gac gcc ctg aag aag     903
377 Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys
378          60                65                70
380 gac aac ggc gag tac acc gtg gac gtg gcc gac aag ggc tac acc ctg     951
381 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu
382 75                80                85                90
385 aac atc aag ttc gcc ggc aag gag aag acc ccc gag gag ccc aag gag     999
386 Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu
387               95               100               105
389 gag gtg acc atc aag gcc aac ctg atc tac gcc gac ggc aag acc cag    1047
390 Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln
391              110               115               120
393 acc gcc gag ttc aag ggc acc ttc gag gag gcc acc gcg gag gcc tac    1095
394 Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr
395          125               130               135
397 cgc tac gcc gac gcc ctg aag aag gac aac ggc gag tac acc gtg gac    1143
398 Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp
399          140               145               150
401 gtg gcc gac aag ggc tac acc ctg aac atc aag ttc gcc ggc aag gag    1191
402 Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu
403 155               160               165               170
406 aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg    1239
407 Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
408              175               180               185
410 atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc    1287
411 Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
412              190               195               200
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VERIFICATION SUMMARY   DATE: 10/22/2001
PATENT APPLICATION: US/09/889,182   TIME: 12:13:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\10222001\I889182.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:750 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:754 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:762 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:766 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:770 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:774 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:778 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:782 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:786 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5